Amendments to the Specification:

Please replace paragraphs [0071], [0104] and [0107] with the following amended paragraphs:

[0071] In relation to polynucleotides and polypeptides, the term substantially identical or homologous or similar varies with the context as understood by those skilled in the relevant art and generally means at least 70%, preferably means at least 80%, more preferably at least 90%, more preferably at least 93%, more preferably at least 95% identity, more preferably at least 96% identity, sometimes at least 97% identity or even at least about 98% identity. To determine identity, optimal alignment of sequences for comparison can be conducted, e.g., by the local homology algorithm of Smith & Waterman, 1981, Adv. Appl. Math. 2:482, by the search for similarity method of Pearson & Lipman, 1988, Proc. Natl. Acad. Sci. USA 85:2444, using the CLUSTAL W algorithm of Thompson et al., 1994, Nucleic Acids Res 22:467380, by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, Wis. The BLAST algorithm (Altschul et al., 1990, Mol. Biol. 215:403-10) for which software may be obtained through the National Center for Biotechnology Information, see BLAST (a service of the National Center for Biotechnology Information, U.S. National Library of Medicine, 8600 Rockville Pike, Bethesda, Md. 20894) [online] program selection revised Apr. 25, 2002 [retrieved on Jun. 26, 2003]. ~~Retrieved from the Internet: <URL:http://www.ncbi.nlm.nih.gov/BLAST/>~~ The BLAST program available at www.ncbi.nlm.nih.gov/BLAST/ can also be used. When using any of the aforementioned algorithms, the default parameters for "Window" length, gap penalty, etc., are used.

[0104] (C) DNA Sequencing and Analysis. PCR-based double-stranded DNA sequencing was performed on a Beckman CEQ 2000 capillary sequencer using reagents and protocols provided by the manufacturer. A shotgun library of the entire cosmid pKOSO79-93D insert was made as follows: DNA was first digested with DraI to eliminate the vector fragment, then partially digested with Sau3AI. After agarose electrophoresis, bands between 1 and 3 kb were excised from the gel and ligated with BamHI digested pUC19. Another shotgun library was generated from a 12 kb XhoI-EcoRI fragment subcloned from cosmid pKOSO79-93A to extend the sequence to the megF gene. A 4 kb BglII-XhoI fragment from cosmid pKOS079-138B was sequenced by primer walking to extend the sequencing to the megBVI gene. Sequence was assembled using the SEQUENCHER (Gene Codes) software package and ~~analysed~~ analyzed with MacVector (Oxford Molecular Group) and the NCBI BLAST server (www.ncbi.nlm.nih.gov/blast/) ~~(http://www.ncbi.nlm.nih.gov/blast/)~~.

[0107] The glycosyl synthase, transfer, and regulatory genes of the upstream region of the meg PKS are contained in the nucleotide sequence SEQ ID NO. ~~No.~~ 1.